

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 17, 2002, 00:35:59 ; Search time 311.51 Seconds
(without alignments)
9882.275 Million cell updates/sec

Title: US-09-719-017a-2
Perfect score: 1793
Sequence: 1 gaattccctgtgacatca.....caattactcaatgccgcg 1793

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues
Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_032802.*
1: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
2: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
3: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
4: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*
5: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.*
6: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.*
7: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.*
8: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.*
9: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.*
10: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.*
11: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.*
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13: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.*
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15: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.*
16: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT.*
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19: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
20: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
21: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
22: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
23: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1793	100.0	1793	21	AAA47190
2	1793	100.0	1793	21	AA245325
3	1126.4	62.8	1727	15	AA086279
4	954.2	53.2	1071	21	AA12173
5	404	22.5	5096	16	AA083824
6	404	22.5	5110	16	AA083833
7	404	22.5	5110	16	AA083834
8	404	22.5	5110	16	AA083835
9	404	22.5	5110	16	AA083836

10	404	22.5	5110	16	AA083825	plasmid PCM-X. S
11	404	22.5	5110	16	AA083826	plasmid PCM-T10-1.
12	404	22.5	5110	16	AA083827	plasmid PCM-T297.
13	404	22.5	5110	16	AA083828	plasmid PCM-p1160.
14	404	22.5	5110	16	AA083829	plasmid PCM-T270.
15	404	22.5	5110	16	AA083830	plasmid PCM-p1087.
16	404	22.5	5110	16	AA083831	plasmid PCM-p1198.
17	404	22.5	5110	16	AA083832	plasmid PCM-r286.
18	403.6	22.5	502	16	AA092246	trnb ribosomal RNA
19	401.6	22.4	7615	20	AA18349	telomerase coding
20	401.6	22.4	7688	20	AA18351	telomerase coding
21	401.6	22.4	7797	20	AA18350	telomerase coding
22	388.4	21.7	4222	10	AA092038	Sequence of recomb
23	388.4	21.7	4466	10	AA090286	plasmid pfp104-4.
24	388.4	21.7	4466	15	AA058637	PTP104-4 sequence.
25	386.8	21.6	4207	10	AA092031	Sequence of recomb
26	385.2	21.5	4204	12	AA010279	Sequence of plasmid
27	336	18.7	5641	22	AA030800	Vector plasmid pJM
28	336	18.7	5670	22	AA030801	Vector plasmid pJM
29	336	18.7	5826	22	AA030798	Vector plasmid pJY
30	336	18.7	6071	22	AA030799	Vector plasmid pJY
31	332.8	18.6	3753	24	ABA04129	plasmid pHE197(II)
32	332.8	18.6	3755	24	ABA04130	plasmid pHE197(II)
33	332.8	18.6	3950	22	AA081854	plasmid pSB-92 nuc
34	332.8	18.6	4176	10	AA090709	Sequence of plasmid
35	332.8	18.6	4214	21	AAA62632	Vector pEP1ink6 D
36	332.8	18.6	4214	21	AAA59260	Nucleotide sequenc
37	332.8	18.6	4357	22	AA031389	Expression vector
38	332.8	18.6	4816	22	AA007799	pTRC15B vector co
39	332.8	18.6	5021	21	AAA07775	DNA sequence of pI
40	332.8	18.6	5027	20	AA078865	Human tissue facto
41	332.8	18.6	5069	20	AA078874	Human tissue facto
42	332.8	18.6	5069	20	AA078871	Human tissue facto
43	332.8	18.6	5099	20	AA078896	Human tissue facto
44	332.8	18.6	5104	22	AA007798	Human tissue facto
45	332.8	18.6	5132	20	AA078883	Human tissue facto

ALIGNMENTS

RESULT 1	
AAAA7190	
ID	AAAA7190 standard; DNA; 1793 BP.
XX	
AC	AAAA7190;
XX	
DT	03-OCT-2000 (first entry)
DE	Nucleotide sequence of the expression cassette of pRPA-BCAT41.
XX	
KW	Methionine; 2-hydroxy-4-methylthiobutanoic acid; nitrilase;
KW	nitrile hydratase; amidase; pRPA-BCAT41; ss.
XX	
OS	Synthetic.
XX	
FH	Key
FT	CDS
FT	Location/Qualifiers
FT	123..1193
FT	/*tag= a
XX	
PN	W0200036120-A1.
XX	
XX	22-JUN-2000.
XX	
PF	10-DEC-1999;
XX	99WO-FR03089.
PR	11-DEC-1998;
PR	98FR-0015849.
XX	19-JUL-1999;
XX	99FR-0009489.
XX	
PA	(RHON) RHONE-POULENC ANIMAL NUTRITION SA.
XX	
PI	Favre-Bulle O, Pierrard J, Batisse Deblitte N;

OY 1741 gctcagcattgtatgtgcgaagacgacacattactcaatgcccgcg 1793
|||||
Db 1741 gctcagcattgtatgtgcgaagacgacacattactcaatgcccgcg 1793

RESULT 2
AAZ45325
ID AAZ45325 standard; DNA: 1793 BP.
XX
AC AAZ45325;
XX
DT 27-MAR-2000 (first entry)
XX
DE Nucleotide sequence of an expression cassette encoding a nitrilase.
XX
KM Tryptophan promoter; P1rp promoter; heterologous protein expression;
KM Escherichia coli W; Industrial protein production; enzyme: nitrilase; ss.
XX
OS Synthetic.
XX Alcaligenes faecalis.
OS
FH Key Location/Qualifiers
FT CDS 123..1193
FT /*tag= a
FT /product= "nitrilase"
XX
XX MO9964607-A1.
XX
XX 16-DEC-1999.
XX
XX 08-JUN-1999; 99MO-FR01343.
XX
XX 10-JUN-1998; 98FR-0007474.
XX
XX (RHON) RHONE-POULENC NUTRITION ANIMALE.
XX
XX Pierrard J, Guitton C, Favre-Bulle O;
XX
XX WPI: 2000-097541/08.
XX
XX P-PSDB: AA154121.
XX
XX Industrial production of heterologous proteins in Escherichia coli
XX strain W, particularly for expressing enzymes -
XX
XX Example 1: Page 36-38; 52pp: French.
XX
XX The present sequence represents an expression cassette comprising
CC the tryptophan promoter (P1rp promoter) and DNA encoding an Alcaligenes
CC faecalis ATCC8750 nitrilase (nitB). The nitrilase polynucleotide and the
CC promoter sequence were extracted from plasmid pRPA6BcAT6 by restriction
CC digest. The P1rp promoter is used to control the expression of a
CC heterologous protein in an expression cassette which is used to modify
CC a strain of Escherichia coli W. The modified strain is then used for
CC industrial production of heterologous proteins. Specifically, the
CC promoter is used to control the expression of an Alcaligenes nitrilase
CC gene. The method is especially used to produce proteins of relatively
XX low value, preferably enzymes and specifically nitrilases.
XX
XX Sequence 1793 BP: 412 A; 527 C; 478 G; 376 T; 0 other;
SQ

Query Match 100.0%; Score 1793; DB 21: Length 1793;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1793: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gattcccggttgacaattaatcagtaactgaactgaactgaactgagcgttgctgcag 60
|||||
Db 1 gattcccggttgacaattaatcagtaactgaactgaactgaactgagcgttgctgcag 60

OY 61 tcgacctgcagccaagcttgcgcatacatcaatcgttatcctcaagaaatactac 120
|||||
Db 61 tcgacctgcagccaagcttgcgcatacatcaatcgttatcctcaagaaatactac 120

OY 121 atatgcagacaagaataaataatcgtccgggcagccgcgttaacaggccgcctctcccaactacg 180
|||||
Db 121 atatgcagacaagaataaataatcgtccgggcagccgcgttaacaggccgcctctcccaactacg 180

OY 181 atctgcgaacaggtgtgtgaataaacattgaagctggtcgttcagggccgcgatagaagct 240
|||||
Db 181 atctgcgaacaggtgtgtgaataaacattgaagctggtcgttcagggccgcgatagaagct 240

OY 241 gtgacctgaatcgtgttggatgaacctggtcgtccggcgtatcccttccagctctggtcgtg 300
|||||
Db 241 gtgacctgaatcgtgttggatgaacctggtcgtccggcgtatcccttccagctctggtcgtg 300

OY 301 ggcgaccggtcgtgtgcgtgaagataagtgccgcgtactatgccaactgcgtcgtcgtg 360
|||||
Db 301 ggcgaccggtcgtgtgcgtgaagataagtgccgcgtactatgccaactgcgtcgtcgtg 360

OY 361 acagtgcaagagtttcaacgcatctgcccgaagccgcgacgaccttggttatcttcatcgcac 420
|||||
Db 361 acagtgcaagagtttcaacgcatctgcccgaagccgcgacgaccttggttatcttcatcgcac 420

OY 421 tgggttatagcagcgcagcgcgcgagccttacccttggtgccaatgctgtatctgcagaca 480
|||||
Db 421 tgggttatagcagcgcagcgcgcgagccttacccttggtgccaatgctgtatctgcagaca 480

OY 481 agggccagatgctgtgtgtcgtcgtcgaacactcaaacctcaatgtttgagcgacgctgt 540
|||||
Db 481 agggccagatgctgtgtgtcgtcgtcgaacactcaaacctcaatgtttgagcgacgctgt 540

OY 541 ttggtgaaggttatgcccagagatctgattgtgtccgacacgagctgggcgcgtcgtgtg 600
|||||
Db 541 ttggtgaaggttatgcccagagatctgattgtgtccgacacgagctgggcgcgtcgtgtg 600

OY 601 cccctgtgtcgttggagacacctgtcccttgagcaagtaacgctgtatctcccaagcacg 660
|||||
Db 601 cccctgtgtcgttggagacacctgtcccttgagcaagtaacgctgtatctcccaagcacg 660

OY 661 aagccatcacatttgcgcgttgcgcgtctcttgcgtgtgaagcgagacgcccacgtgc 720
|||||
Db 661 aagccatcacatttgcgcgttgcgcgtctcttgcgtgtgaagcgagacgcccacgtgc 720

OY 721 tcagcccaaggttgaacatgagctgctcgcgaataatcattcgtgttgaagccagtgctta 780
|||||
Db 721 tcagcccaaggttgaacatgagctgctcgcgaataatcattcgtgttgaagccagtgctta 780

OY 781 ccatgcgcgcagcaagtgtcgttcacccagagacatgacatgctggaagtgtgaac 840
|||||
Db 781 ccatgcgcgcagcaagtgtcgttcacccagagacatgacatgctggaagtgtgaac 840

OY 841 acaagcctccctgctggaagtggtggtgcgagcttcacatgattttgcccgaagagac 900
|||||
Db 841 acaagcctccctgctggaagtggtggtgcgagcttcacatgattttgcccgaagagac 900

OY 901 gcaatgtgctcctcctaccgcgacacagatgcggaagctgcatctgcatctgaataa 960
|||||
Db 901 gcaatgtgctcctcctaccgcgacacagatgcggaagctgcatctgcatctgaataa 960

OY 961 tgggaagaaattgcttcgcgcgaagcgatcaacgacctgttggccactactccaaacccg 1020
|||||
Db 961 tgggaagaaattgcttcgcgcgaagcgatcaacgacctgttggccactactccaaacccg 1020

OY 1021 aggcacccgctctgtgtactgcgagcttgggacgcgtgagcccatgactcgggtgcatcca 1080
|||||
Db 1021 aggcacccgctctgtgtactgcgagcttgggacgcgtgagcccatgactcgggtgcatcca 1080

OY 1081 aaagcgtgtatccaggaagaagctcccgagccgacgttgcaaaagtacggtcgtgccgtgtg 1140
|||||
Db 1081 aaagcgtgtatccaggaagaagctcccgagccgacgttgcaaaagtacggtcgtgccgtgtg 1140

OY 1141 ccgttcagcagactcagacatcgatcgtactggttgcaaaacgctctctgaccccaaa 1200
|||||
Db 1141 ccgttcagcagactcagacatcgatcgtactggttgcaaaacgctctctgaccccaaa 1200

```

QY 1201 agatgcaagggccgggcaaaactgtccggctcttgatctctctcgtccggatccact 1260
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DB 1201 agatgcaagggccgggcaaaactgtccggctcttgatctctctcgtccggatccact 1260
QY 1261 agtctagaagtcgaactgcagcagcatggaactgggtcccaacttgaccatgcccgaact 1320
    |||||||
DB 1261 agtctagaagtcgaactgcagcagcatggaactgggtcccaacttgaccatgcccgaact 1320
QY 1321 caaagaatgaaacgcgttagcgccgatgtgtagtgggtgtctcccaatgcagagtaaggga 1380
    |||||||
DB 1321 cagaagaatgaaacgcgttagcgccgatgtgtagtgggtgtctcccaatgcagagtaaggga 1380
QY 1381 actgcagagcatcaataaagaagaagctcagtcgaagaacttgggcttcgtttatc 1440
    |||||||
DB 1381 actgcagagcatcaataaagaagaagctcagtcgaagaacttgggcttcgtttatc 1440
QY 1441 tgtgtgttgcgttgaaagctcctcctgagtaggaacaatccggcggaagagattgaac 1500
    |||||||
DB 1441 tgtgtgttgcgttgaaagctcctcctgagtaggaacaatccggcggaagagattgaac 1500
QY 1501 gtgcgaagcaagcgccgggaagggtgtagcgagcaggaagcgcgcataaactgcagagcat 1560
    |||||||
DB 1501 gtgcgaagcaagcgccgggaagggtgtagcgagcaggaagcgcgcataaactgcagagcat 1560
QY 1561 caaattagaagaagaagcctcctgaagcagatggccttttgcgtttctcaaaactctcct 1620
    |||||||
DB 1561 caaattagaagaagaagcctcctgaagcagatggccttttgcgtttctcaaaactctcct 1620
QY 1621 gtgcgtatatactaaagccatcccccacagatacagtaaacctgcttttgcgtc 1680
    |||||||
DB 1621 gtgcgtatatactaaagccatcccccacagatacagtaaacctgcttttgcgtc 1680
QY 1681 aggaagaagcagctatgaaacacatccttaaaacccctggaacaacatttggcattgataat 1740
    |||||||
DB 1681 aggaagaagcagctatgaaacacatccttaaaacccctggaacaacatttggcattgataat 1740
QY 1741 ggtcgaacacattgatgtgtagcggaagaacgaacaattactcaatggccgcgg 1793
    |||||||
DB 1741 ggtcgaacacattgatgtgtagcggaagaacgaacaattactcaatggccgcgg 1793

RESULT 3
AA086279
ID AA086279 standard; DNM: 1727 BP.
AC AA086279:
XX
XX 12-AUG-1999 (first entry)
DT
XX
DE Nitrilase enzyme coding sequence.
XX
KW Nitrilase; organic acid preparation; nitrile compound hydrolysis;
KW amide production; carboxylic acid production; ss.
XX
OS Alcaligenes faecalis.
XX
XX JP06153968-A.
XX
XX 03-JUN-1994.
PD
XX
XX 17-NOV-1992: 92JP-0306663.
PF
XX
XX 17-NOV-1992: 92JP-0306663.
PR
XX
XX (NITTO ) NITTO CHEM IND CO LTD.
PA
XX
XX MPI: 1994-220515/27.
DR
XX
XX P-PSDB; AAR61104.
DR
XX
XX Organic acid prepn by hydrolysing nitrile - using nitrilase enzyme
PT obtd from transformed organism.
XX
XX Claim 1: Fig 2: 9pp; Japanese.
PS

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XX
CC This sequence encodes the nitrilase enzyme from Alcaligenes faecalis.
CC The invention relates to a method of preparing organic acid by
CC hydrolysing nitrile compounds of formula R1CH(R2)CN with nitrilase to
CC form carboxylic acid of formula R1CH(R2)COOH and equimolar amount of
CC ammonia. (R1 is optionally substituted phenyl, naphthyl, indole,
CC thiophene, pyridyl or cyclohexenyl; R1 is H or hydroxyl group). The
CC nitrilase is prepared by culturing a transformant containing recombinant
CC DNA obtained by integrating into a vector the A. faecalis nitrilase
CC enzyme DNA. Various kinds of amide or carboxylic acid can be produced
CC industrially in good efficiency.
SQ
Sequence 1727 BP; 343 A; 566 C; 468 G; 350 T; 0 other;

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Query Match 62.8%; Score 1126.4; DB 15; Length 1727;
Best Local Similarity 99.5%; Pred. No. 3.5e-234;
Matches 1130; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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```

QY 122 tatgcagacagaanaaaatcgtccgggagcgccgttacaggccgctctcccaactaga 181
    |||||||
DB 122 tatgcagacagaanaaaatcgtccgggagcgccgttacaggccgctctcccaactaga 181
QY 303 tatgcagacagaanaaaatcgtccgggagcgccgttacaggccgctctcccaactaga 362
    |||||||
DB 303 tatgcagacagaanaaaatcgtccgggagcgccgttacaggccgctctcccaactaga 362
QY 182 tctggcaagcggtgttataaacaattgagctggtcgtcagggccggcagatgaaggctg 241
    |||||||
DB 182 tctggcaagcggtgttataaacaattgagctggtcgtcagggccggcagatgaaggctg 241
QY 363 tctggcaagcggtgttataaacaattgagctggtcgtcagggccggcagatgaaggctg 422
    |||||||
DB 363 tctggcaagcggtgttataaacaattgagctggtcgtcagggccggcagatgaaggctg 422
QY 242 tgaactgatcgtgttgtttaaacttgcgtgcgcgcgtacatcccttcacagctcgtgcgg 301
    |||||||
DB 242 tgaactgatcgtgttgtttaaacttgcgtgcgcgcgtacatcccttcacagctcgtgcgg 301
QY 423 tgaactgatcgtgttgtttaaacttgcgtgcgcgcgtacatcccttcacagctcgtgcgg 482
    |||||||
DB 423 tgaactgatcgtgttgtttaaacttgcgtgcgcgcgtacatcccttcacagctcgtgcgg 482
QY 302 cgcacgcgcgtgtcgtgtaataaagtcgcgcgtactatgcaaatcgcgtcgtcgtga 361
    |||||||
DB 302 cgcacgcgcgtgtcgtgtaataaagtcgcgcgtactatgcaaatcgcgtcgtcgtga 361
QY 483 cgcacgcgcgtgtcgtgtaataaagtcgcgcgtactatgcaaatcgcgtcgtcgtga 542
    |||||||
DB 483 cgcacgcgcgtgtcgtgtaataaagtcgcgcgtactatgcaaatcgcgtcgtcgtga 542
QY 362 cagtcgaagatttcaagcacttcccgagcgccagcagcacttggatttcaactgact 421
    |||||||
DB 362 cagtcgaagatttcaagcacttcccgagcgccagcagcacttggatttcaactgact 421
QY 543 cagtcgaagatttcaagcacttcccgagcgccagcagcacttggatttcaactgact 602
    |||||||
DB 543 cagtcgaagatttcaagcacttcccgagcgccagcagcacttggatttcaactgact 602
QY 422 gggttatagcagcgagcagcgcgagccttcaacttgcgttgcgaatgctgaacga 481
    |||||||
DB 422 gggttatagcagcgagcagcgcgagccttcaacttgcgttgcgaatgctgaacga 481
QY 603 gggttatagcagcgagcagcgcgagccttcaacttgcgttgcgaatgctgaacga 662
    |||||||
DB 603 gggttatagcagcgagcagcgcgagccttcaacttgcgttgcgaatgctgaacga 662
QY 482 gggcagagatcgtgtgtcgcgttcgcaaatcctaactcaacatggttgaagcagcggtgt 541
    |||||||
DB 482 gggcagagatcgtgtgtcgcgttcgcaaatcctaactcaacatggttgaagcagcggtgt 541
QY 663 gggcagagatcgtgtgtcgcgttcgcaaatcctaactcaacatggttgaagcagcggtgt 722
    |||||||
DB 663 gggcagagatcgtgtgtcgcgttcgcaaatcctaactcaacatggttgaagcagcggtgt 722
QY 542 tgttgaaggttatgcccgaagatcgtgtgttgcgaacacgagctggcgctgctgc 601
    |||||||
DB 542 tgttgaaggttatgcccgaagatcgtgtgttgcgaacacgagctggcgctgctgc 601
QY 723 tgttgaaggttatgcccgaagatcgtgtgttgcgaacacgagctggcgctgctgc 782
    |||||||
DB 723 tgttgaaggttatgcccgaagatcgtgtgttgcgaacacgagctggcgctgctgc 782
QY 602 cctgtgtcgttggagagcacttgcctccttgagaagaatgacgagctgtactccagaacga 661
    |||||||
DB 602 cctgtgtcgttggagagcacttgcctccttgagaagaatgacgagctgtactccagaacga 661
QY 783 cctgtgtcgttggagagcacttgcctccttgagaagaatgacgagctgtactccagaacga 842
    |||||||
DB 783 cctgtgtcgttggagagcacttgcctccttgagaagaatgacgagctgtactccagaacga 842
QY 662 agccatcacaattgcgcgcgtgcgttccttgcgtgtacaagcaaaagcccatgcgct 721
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DB 662 agccatcacaattgcgcgcgtgcgttccttgcgtgtacaagcaaaagcccatgcgct 721
QY 843 agccatcacaattgcgcgcgtgcgttccttgcgtgtacaagcaaaagcccatgcgct 902
    |||||||
DB 843 agccatcacaattgcgcgcgtgcgttccttgcgtgtacaagcaaaagcccatgcgct 902
QY 722 cagcgccaaggtgaaacatgagctccttcgcaaaactatctggttgaagcagctgttac 781
    |||||||
DB 722 cagcgccaaggtgaaacatgagctccttcgcaaaactatctggttgaagcagctgttac 781
QY 903 cagcgccaaggtgaaacatgagctccttcgcaaaactatctggttgaagcagctgttac 962
    |||||||
DB 903 cagcgccaaggtgaaacatgagctccttcgcaaaactatctggttgaagcagctgttac 962
QY 782 catcgccgacagatgctgttcaaccagagacacttgaacatgctgtgaagtaaggtaaca 841
    |||||||
DB 782 catcgccgacagatgctgttcaaccagagacacttgaacatgctgtgaagtaaggtaaca 841
QY 963 catcgccgacagatgctgttcaaccagagacacttgaacatgctgtgaagtaaggtaaca 1022
    |||||||
DB 963 catcgccgacagatgctgttcaaccagagacacttgaacatgctgtgaagtaaggtaaca 1022
QY 842 caacgctcctcgtcgtgaagaatggggcgagcttccatgaaatttgcgcggaaggag 901
    |||||||
DB 842 caacgctcctcgtcgtgaagaatggggcgagcttccatgaaatttgcgcggaaggag 901
QY 1023 caacgctcctcgtcgtgaagaatggggcgagcttccatgaaatttgcgcggaaggag 1082
    |||||||
DB 1023 caacgctcctcgtcgtgaagaatggggcgagcttccatgaaatttgcgcggaaggag 1082
QY 902 caacgctcctcgtcgtgaagaatggggcgagcttccatgaaatttgcgcggaaggag 961
    |||||||
DB 902 caacgctcctcgtcgtgaagaatggggcgagcttccatgaaatttgcgcggaaggag 961

```

Db 1083 cacattgctccctactcgtccacacagatgcgaagcctgatactatctgcgatctgaacat 1142
Qy 962 ggaagaattgctcttcgccaagcgatcaagaccctgtggccactactccaaccgga 1021
Db 1143 ggaagaattgctcttcgccaagcgatcaagaccctgtggccactactccaaccgga 1202
Qy 1022 ggcacccgctgtgtaactggagaccttggcacccgttgagcccatgtgactgggtatccaa 1081
Db 1203 ggcacccgctgtgtaactggagaccttggcacccgttgagcccatgtgactgggtatccaa 1262
Qy 1082 aagcgtgataccaagaagaagctcccgagccgacgltgcaaaagtacggtcgcccgctgc 1141
Db 1263 aagcgtgataccaagaagaagctcccgagccgacgltgcaaaagtacggtcgcccgctgc 1322
Qy 1142 cgtacgacagactcaagactcggatacgtactggtgcaagaacgcgtccctgaaccctaaa 1201
Db 1323 cgtacgacagactcaagactcggatacgtactggtgcaagaacgcgtccctgaaccctaaa 1382
Qy 1202 gatgacaagcgcgggcaaacgtgtcgggttctgattctcttcgtcccgagatcc 1257
Db 1383 gatgacaagcgcgggcaaacgtgtcgggttctgattctcttcgtcccgagatcc 1438

RESULT 4

AA12173
ID AA12173 standard; DNA: 1071 BP.

AC AA12173;

DT 10-AUG-2000 (first entry)

DE A. faecalis nitrilase DNA.

KM Nitrilase: chiral carboxylic acid; racemic nitrile; pharmaceutical;

KW plant protection agent; ds:

OS Alcaligenes faecalis.

PN DE19848129-A1.

PD 20-APR-2000.

PF 19-OCT-1998; 98DE-1048129.

PR 19-OCT-1998; 98DE-1048129.

PA (BAD I) BASF AG.

PI Rees-Loeschke M, Friedrich T, Hauer B, Mattes R, Engels D;

DR WPI: 2000-319322/28.

P-PSDB; AA187649.

XX New nucleic acid sequence encoding Alcaligenes faecalis nitrilase
PT polypeptide useful for converting racemic nitriles to chiral carboxylic
PR acids

PS Claim 1a: Page 14-16; 28pp; German.

XX This invention describes a novel nucleic acid sequence (I) encoding an
CC Alcaligenes faecalis nitrilase polypeptide. The polypeptide encoded by
CC (I), or a growing, resting or digested microorganism containing (I) is
CC useful for preparing chiral carboxylic acids (III) by conversion of
CC racemic nitriles (IV). (III) are useful as intermediates, e.g. for
CC pharmaceuticals and plant protection agents. This sequence encodes the
CC Alcaligenes faecalis nitrilase described in the method of the invention.

XX Sequence 1071 BP: 230 A; 318 C; 304 G; 219 T; 0 other:

Query Match 53.2%; Score 954.2; DB 21; Length 1071;
Best Local Similarity 93.2%; Pred. No. 5.4e-197;
Matches 998; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

Qy 123 atgcagacaagaataatcgtccggcagccgcgtacagagccgcctctcccaactagat 182
Db 1 atgcagacaagaataatcgtccggcagccgcgtacagagccgcctctcccaactagat 60
Qy 183 ctgcgaacgggtgtgtgataaaacattagactggtctgtcaaggcccgatgaaggcgt 242
Db 61 ctgcgaacgggtgtgtgataaaacattagactggtctgtcaaggcccgatgaaggcgt 120
Qy 243 gacctgatacgtgtgtgtgataaaacctgtgccccgtctatcccttccacgtctgtggtgc 302
Db 121 gacctgatacgtgtgtgtgataaaacctgtgccccgtctatcccttccacgtctgtggtgc 180
Qy 303 gcaacgccttggtgtgtgataaaacctgtgccccgtctatcccttccacgtctgtggtgc 362
Db 181 gcaacgccttggtgtgtgataaaacctgtgccccgtctatcccttccacgtctgtggtgc 240
Qy 363 agtcagagattccaacgcatctgccccagccgacagagacctgtgatttccatctgactg 422
Db 241 agtcagagattccaacgcatctgccccagccgacagagacctgtgatttccatctgactg 300
Qy 423 ggtataagcagcgcagcgcgcgcagccttaccctgggccaatgacctgatacagacaag 482
Db 301 ggtataagcagcgcagcgcgcgcagccttaccctgggccaatgacctgatacagacaag 360
Qy 483 ggcacagatgctgt 542
Db 361 ggcacagatgctgt 420
Qy 543 ggtgaaggtatgtcccgagatctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 602
Db 421 ggtgaaggtatgtcccgagatctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 480
Qy 603 ctgt 662
Db 481 ctgt 540
Qy 663 gccattcaacattgcccgtccgtgccccttctgtgtgtgtgtgtgtgtgtgtgtgtgtgt 722
Db 541 gccattcaacattgcccgtccgtgccccttctgtgtgtgtgtgtgtgtgtgtgtgtgtgt 600
Qy 723 agcgcacaagtgtacaatgctgtccctgcgaatactatctgtgtgaaggcagtgcttacc 782
Db 601 agtgcacaagtgtacaatgctgtccctgcgaatactatctgtgtgaaggcagtgcttacc 660
Qy 783 atgcgcgcagcagtgctgt 842
Db 661 atgcgcgcagcagtgctgt 720
Qy 843 aagcctccctgt 902
Db 721 aagcctccctgt 780
Qy 903 acattggtcccttacccttccacacgattgcgcgaagccgcatctatgcccagatgtgaac 962
Db 781 acattggtcccttacccttccacacgattgcgcgaagccgcatctatgcccagatgtgaac 840
Qy 963 gaagaattgctctgcgaagcgatcaacgacctgtgtggccactactccaaccgag 1022
Db 841 gaagaattgctctgcgaagcgatcaacgacctgtgtggccactactccaaccgag 900
Qy 1023 gccaccgctgt 1082
Db 901 gccaccgctgt 960
Qy 1083 agcgtgataccaagaagcctcccgagccgcagcgtgtgcaaaagtacggcgtgcgcgtcc 1142
Db 961 agcgtgataccaagaagcctcccgagccgcagcgtgtgcaaaagtacggcgtgcgcgtcc 1020
Qy 1143 gtcagccaagactcaggaactcggatagcgtactgtgtgcaagaacgctcctga 1193
Db 1021 atcagcattccacagagactcggacacactgctagtcgcaagaagcgcgtcttga 1071

RESULT	5	
AAQ83824		
ID	AAQ83824	standard; DNA; 5096 BP.
XX		
AC	AAQ83824;	
XX		
DT	04-OCT-1995	(first entry)
XX		
DE	Plasmid PKK232-8.	
XX		
KW	Plasmid PKK232-8; bacteriophage T7; RNA polymerase;	
XX	mutant promoters; circular; cyclic; ds.	
XX		
OS	Synthetic.	
XX		
PH	Key	Location/Qualifiers
FT	misc_feature	177..212
FT	/*tag=	a
FT	/note=	"Cloning polylinker prior to a promoterless chloramphenicol acetyl transferase gene"
XX		
PN	US5385834-A.	
XX		
PD	31-JAN-1995.	
XX		
PF	13-AUG-1993;	93US-0106433.
XX		
PR	13-AUG-1993;	93US-0106433.
XX		
PA	(GEOR-) GEORGIA TECH RES CORP.	
XX		
PI	Ikada RA;	
XX		
DR	WPI; 1995-081565/11.	
XX		
PT	New mutant form of T7 RNA polymerase - able to utilise a wide	
PT	range of T7 promoter sequences having mutations that inactivate	
PT	recognition by wild type enzyme	
XX		
PS	Disclosure; Columns 37-42; 79pp; English.	
XX		
CC	AAQ83824 is the plasmid PKK232-8. It was used in the production of	
CC	claimed bacteriophage T7 RNA polymerase mutant promoters.	
XX		
SO	Sequence 5096 BP; 1294 A; 1290 G; 1222 T; 0 other;	

Query Match	22.5%	Score 404	DB 16	Length 5096
Best Local Similarity	96.5%	Pred. No. 4.9e-78		
Matches 413	Conservative 0	Mismatches 15	Indels 0	Gaps 0
OY 1267	agagtcgacgacctcagcagcatgcagacgtcttggtctccaccctgaccacatgcgcgaactcgaag	1326		
Db 1237	agaatttgctctggtcggcgcagtaagcgcgtctgtctccacctgcaccatgcccgaactcgaag	1296		
OY 1327	tgaaacgcgcgtatgcgcgcgagatgtaagtgtgtgtgtctctcccatctgagagatagagaaatgcc	1386		
Db 1297	tgaaacgcgcgtatgcgcgcgagatgtaagtgtgtgtgtctctcccatctgagagatagagaaatgcc	1356		
OY 1387	aggcatcaaatataaaccgaaaggctcagtcgaaagacttggtgcctctcgttttatctgtgt	1446		
Db 1357	aggcatcaaatataaaccgaaaggctcagtcgaaagacttggtgcctctcgttttatctgtgt	1416		
OY 1447	ttgtctgtgtgaaagcctctcctctgtatgttgataaatactcgccgggtgcggatcttgaagcttggtg	1506		
Db 1417	ttgtctgtgtgaaagcctctcctctgtatgttgataaatactcgccgggtgcggatcttgaagcttggtg	1476		
OY 1507	aagcaacgccccgggggtgtggtgcgcgcagagacccccgcataacatgcgcagatccaat	1566		
Db 1477	aagcaacgccccgggggtgtggtgcgcgcagagacccccgcataacatgcgcagatccaat	1536		
OY 1567	aagcaagagggcatctccttgcagatgtgcctcttctgtcgtttctctcaaatcttctcgtctc	1626		

Accession	Sequence	Position
Db	1537 aagcgaagagccaccctgaagatgagctctttggcttctctaaaccttcctctgctc	1596
Qy	1627 atatctacaagccatccccccacagatagcgttaactagcctcgtttttgcatcagaaa	1686
Db	1597 atattcaacagccatccccccacagatagcgttaactagcctcgtttttgcatcagaaa	1656
Qy	1687 gcaagctat	1694
Db	1657 gcaagctctg	1664

	RESULT	6
AAQ83833	ID	AAQ83833 standard; DNA: 5110 BP.
XX		
AC		AAQ83833;
XX		
XX		
DT		05-0CT-1995 (first entry)
XX		
DE		Plasmid PCM-B64.
XX		
KM		Plasmid PCM-B64; bacteriophage T7; RNA polymerase;
KM		mutant -8T to C; T7 promoter phi 10; circular; cyclic; ds.
XX		
OS		Synthetic.
XX		
XX		
FH	Key	Location/Qualifiers
FT	Promoter	198..220
FT		/*tag= "a
FT		/note= "intermediate T7 promoter phi 10 mutant (-8T
FT		to C) prior to a promoterless chloramphenicol
FT		acetyl transferase gene"

XX
 PD 31-JAN-1995.
 XX
 PF 13-AUG-1993; 93US-0106433.
 XX
 PR 13-AUG-1993; 93US-0106433.
 XX
 PA (GEOR-) GEORGIA TECH RES CORP.
 XX
 PI Ikeda RA;
 XX
 DR WPI; 1995-081565/11.
 XX
 XX
 PT New mutant form of T7 RNA polymerase - able to utilise a wide
 PT range of T7 promoter sequences having mutations that inactivate
 PT recognition by wild type enzyme
 XX
 PS
 XX Disclosure; Columns 97-104; 79pp; English.
 XX
 CC AO83833 is the plasmid pCM-B64, it was used in the production of
 CC the bacteriophage T7 RNA polymerase mutant promoter phi 10 -8T
 CC to C substitution (claimed).
 XX
 SQ Sequence 5110 BP; 1305 A; 1289 C; 1289 G; 1227 T; 0 other;

Query Match	22.5%	Score 404	DB 16	Length 5110
Best Local Similarity	96.5%	Pred. No. 4.9e-78		
Matches 413	Conservative 0	Mismatches 15	Indels 0	Gaps 0
QY 1267	agaatgcgaactgcaggaatgcgaagcttggtcccaactgaccccatgcgaactagaag			1326
Db 1251	agaattgctctggcgcaatgcagtcgcggtctgccactgaccccatgycgaactagaag			1310
QY 1327	tgaaacgcctgatgcgcgcgatgtatgttgggtctccccaatgcgagatgaagaaactgc			1386
Db 1311	tgaacgcctgatgcgcgcgatgtatgttgggtctccccaatgcgagatgaagaaactgc			1370

XX	AAO83834 standard; DNA; 5110 BP.
XX	AAO83834;
XX	05-OCT-1995 (first entry)
XX	Plasmid PCM-P1208.
KW	plasmid pcm-p1208; bacteriophage T7; RNA polymerase;
KM	mutant -7C to G; T7 promoter phi 10; circular; cyclic; ds.
XX	Synthetic.
OS	
XX	Key
FH	Location/Qualifiers
FT	Promoter 198..220
FT	/tag= a
FT	/note= "inactive T7 promoter phi 10 mutant (-7C to
FT	G) prior to a promoterless chloramphenicol
FT	acetyl transferase gene"
PN	US5385834-A.
XX	
PD	31-JAN-1995.
XX	
XX	13-AUG-1993; 93US-0106433.
PE	
XX	
PR	13-AUG-1993; 93US-0106433.
XX	
PA	(GEOR-) GEORGIA TECH RES CORP.
XX	
PI	Ikedo RA;
DR	
XX	WPI; 1995-081565/11.
PT	
PT	New mutant form of T7 RNA polymerase - able to utilise a wide
PT	range of T7 promoter sequences having mutations that inactivate
XX	recognition by wild type enzyme
PS	
XX	Disclosure; Columns 105-110; 79pp; English.
CC	AAO83834 is the plasmid pcm-p1208, it was used in the production of
CC	the bacteriophage T7 RNA polymerase mutant promoter phi 10 -7C
CC	to G substitution (claimed).
XX	
XQ	Sequence 5110 BP; 1305 A; 1288 C; 1290 G; 1227 T; 0 other;

[illegible]

XX	RESULT	8
XX	AAQ83835	
XX	AAQ83835	standard; DNA; 5110 BP.
XX	AC	
XX	AAQ83835;	
XX	06-OCT-1995	(first entry)
XX	DE	
XX	Plasmid	PCM-P1031.
XX	Plasmid	PCM-P1031; bacteriophage T7; RNA polymerase;
XX	mutant	-7C to A; T7 promoter phi 10; circular; cyclic; ds.
XX	Synthetic.	
XX	OS	
XX	Key	Location/Qualifiers
XX	Promoter	198..220
XX	FT	/*tag= a
XX	FT	/note= "inactive T7 promoter phi 10 mutant (-7C to
XX	FT	A) prior to a promoterless chloramphenicol
XX	FT	acetyl transferase gene"
XX	PN	US5385834-A.
XX	PD	31-JAN-1995.
XX	PP	13-AUG-1993; 93US-0106433.
XX	PR	13-AUG-1993; 93US-0106433.
XX	PA	(GEOR-) GEORGIA TECH RES CORP.
XX	PI	Ikeda RA;
XX	WP1; 1995-081565/11.	

XX New mutant form of T7 RNA polymerase - able to utilise a wide
PT range of T7 promoter sequences having mutations that inactivate
PT recognition by wild type enzyme
XX
PS Disclosure; Columns 111-118; 79pp; English.
XX
CC-AA083835 is the plasmid pCM-P1031, it was used in the production of
CC the bacteriophage T7 RNA polymerase mutant promoter phi 10 -7C
CC to A substitution (claimed).
XX
XQ Sequence 5110 BP; 1306 A; 1286 C; 1290 G; 1228 T; 0 other;

Query Match	22.5%	Score 404;	DB 16;	Length 5110;
Best Local Similarity	96.5%;	Pred. No. 4.9e-78;		
Matches 413; Conservative	0;	Mismatches 15;	Indels 0;	Gaps 0;

QY	1267	agaaatcgaacccgagcgatcgaagccttgggtctccacatgaacccaatgcggaactcagaag	1326
Db	1261	agaaatctgcctctgctgagcgagtaagcgcggctggctccacatgaacccaatgcggaactcagaag	1310
QY	1327	tgaaacgcgcgttaagcgcgcgaatggtgtatgtctgggtgtctcccaatgagaaatgaagaaatcgc	1386
Db	1311	tgaaacgcgcgttaagcgcgcgaatggtgtatgtctgggtgtctcccaatgagaaatgaagaaatcgc	1370
QY	1387	aggaatcaaaataaagaagaaggtctgaagtcgaaagaatctgggccttctcgctttatctgctgt	1446
Db	1371	aggaatcaaaataaagaagaaggtctgaagtcgaaagaatctgggccttctcgctttatctgctgt	1430
QY	1447	ctgtcctgttgaaacgcctctccctcgaatgaagacaataatccgcggagcggaatttgaaacgttcg	1506
Db	1431	ctgtcctgttgaaacgcctctccctcgaatgaagacaataatccgcggagcggaatttgaaacgttcg	1490
QY	1507	aagcaacgcgcctccggagaggtgtgcggcgagaagcgcgcgcataaactgtccagagcatcaaat	1566
Db	1491	aagcaacgcgcctccggagaggtgtgcggcgagaagcgcgcgcataaactgtccagagcatcaaat	1550
QY	1567	aagcagaagaagccatctccgagaagatgtgccttttgcgtttctcaaacctcttcctgtctc	1626
Db	1551	aagcagaagaagccatctccgagaagatgtgccttttgcgtttctcaaacctcttcctgtctc	1610
QY	1627	ataatctacaagccatctcccccacagaatacgttaaaatagcctcgtcttttgcatacaggaaa	1686
Db	1611	ataatctacaagccatctcccccacagaatacgttaaaatagcctcgtcttttgcatacaggaaa	1670
QY	1687	gcagctat 1694	
Db	1671	gcagctat 1678	

RESULT	9
AAQ83836	
ID	AAQ83836 standard; DNA; 5110 BP.

AC AAQ83836;

DT 06-OCT-1995 (first entry)

DE Plasmid PCM-T221.

KW Plasmid pcm-T221; bacteriophage T7; RNA polymerase;
KW mutant -6A to G; T7 promoter ph1 10; circular; ds.

05 Synthetic.

FH	Key	Location/Qualifiers
FT	Promoter	198..220

PN USS385634-A.
XX
PD 31-JAN-1995.
XX
XX 13-AUG-1993; 93US-0106433.
XX PF
XX 13-AUG-1993; 93US-0106433.
XX PR
XX (GEOR-) GEORGIA TECH RES CORP.
PA
XX
PI Ikeda RA;
XX
XX
DR WPI: 1995-081565/11.
XX
XX New mutant form of T7 RNA polymerase - able to utilise a wide
PT range of T7 promoter sequences having mutations that inactivate
PT recognition by wild type enzyme
XX
XX
PS Disclosure: Columns 119-124; 79pp; English.
XX
XX
CC AA083836 is the plasmid pcm-T221, it was used in the production of
CC the bacteriophage T7 RNA polymerase mutant promoter phi 10 -6a
CC to G substitution (claimed).
XX
SQ Sequence 5110 BP; 1304 A; 1288 C; 1290 G; 1228 T; 0 other;

Query Match	22.5%	Score 404;	DB 16;	Length 5110;
Best Local Similarity	96.5%;	Pred. No. 4.9e-78;		
Matches 413;	Conservative 0;	Mismatches 15;	Indels 0;	Gaps 0;

[illegible]

RESULT	10
AAQ83825	
ID	AAQ83825 standard; DNA; 5110 BP

AC AAQ838257

DT 04-OCT-1995 (first entry)

DE Plasmid pCM-X#


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XX Plasmid pcm-x#: bacteriophage T7; RNA polymerase:
KW mutant promoters; circular; cyclic; ds.
XX Synthetic.
OS Key Location/Qualifiers
XX FH Promoter 198..220
FT /tag=^a
FT /note="potential T7 promoter prior to a promoterless
FT chloramphenicol acetyl transferase gene"
XX US5385834-A.
XX 31-JAN-1995.
XX 13-AUG-1993; 93US-0106433.
XX 13-AUG-1993; 93US-0106433.
XX (GEOR-) GEORGIA TECH RES CORP.
XX PA
XX PI Ikeda RA;
XX DR WPI; 1995-081565/11.
XX PT New mutant form of T7 RNA polymerase - able to utilise a wide
PT range of T7 promoter sequences having mutations that inactivate
PT recognition by wild type enzyme
XX PS Disclosure; Columns 43-50; 79pp; English.
XX CC AA083825 is the plasmid pcm-x#, it was used in the production of
CC claimed bacteriophage T7 RNA polymerase mutant promoters.
XX SX Sequence 5110 BP; 1303 A; 1287 C; 1288 G; 1226 T; 6 other;

Query Match 22.5%; Score 404; DB 16; Length 5110;
Best Local Similarity 96.5%; Pred. No. 4.9e-78;
Matches 413; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1267 agagtcgacctgcaagcagcttggtgtccacatgacccatgcccgaactcagaag 1326
DB 1251 agaattgcttgctgagcagtagcggtgtgtccacatgacccatgcccgaactcagaag 1310
QY 1327 tgaacgcgtagcgccgtagtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1386
DB 1311 tgaacgcgtagcgccgtagtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1370
QY 1387 aggcatacaataaagaaggtcagtcgaaagacttggtgtgtgtgtgtgtgtgtgtgtgt 1446
DB 1371 aggcatacaataaagaaggtcagtcgaaagacttggtgtgtgtgtgtgtgtgtgtgtgt 1430
QY 1447 ttgtcgtgaacgctctcctgtagtagacaatccgcgcggagcgagattgaacgttgcg 1506
DB 1431 ttgtcgtgaacgctctcctgtagtagacaatccgcgcggagcgagattgaacgttgcg 1490
QY 1507 aagcaacgcccggaggtgtgcggtgagcagccgcataaactgtccaggtcacaatt 1566
DB 1491 aagcaacgcccggaggtgtgcggtgagcagccgcataaactgtccaggtcacaatt 1550
QY 1567 aagcagaagcgcattcctgtagtagcgttttgcgttttctaactcttctgtcgctc 1626
DB 1551 aagcagaagcgcattcctgtagtagcgttttgcgttttctaactcttctgtcgctc 1610
QY 1627 atatacaacagcattccccacacagatacgttaactagcctgttttgcacatgagaa 1686
DB 1611 atatacaacagcattccccacacagatacgttaactagcctgttttgcacatgagaa 1670
QY 1687 gcaagctat 1694
DB 1671 gcaagctgt 1678

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RESULT 11
AA083826
ID AA083826 standard; DNA; 5110 BP.
XX
XX AA083826;
AC
XX 04-OCT-1995 (first entry)
XX
XX Plasmid pCAT10-1.
XX
XX Plasmid pCAT10-1; bacteriophage T7; RNA polymerase;
KW mutant promoters; circular; cyclic; T7 promoter phi 10; ds.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX FH misc_feature 198..220
FT /tag=^a
FT /note="T7 promoter phi 10 prior to a promoterless
FT chloramphenicol acetyl transferase gene"
XX US5385834-A.
XX 31-JAN-1995.
XX 13-AUG-1993; 93US-0106433.
XX 13-AUG-1993; 93US-0106433.
XX (GEOR-) GEORGIA TECH RES CORP.
XX PA
XX PI Ikeda RA;
XX DR WPI; 1995-081565/11.
XX PT New mutant form of T7 RNA polymerase - able to utilise a wide
PT range of T7 promoter sequences having mutations that inactivate
PT recognition by wild type enzyme
XX PS Disclosure; Columns 51-56; 79pp; English.
XX CC AA083826 is the plasmid pCAT10-1, it was used in the production of
CC the bacteriophage T7 RNA polymerase promoter phi 10.
XX SX Sequence 5110 BP; 1305 A; 1288 C; 1289 G; 1228 T; 0 other;

Query Match 22.5%; Score 404; DB 16; Length 5110;
Best Local Similarity 96.5%; Pred. No. 4.9e-78;
Matches 413; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1267 agagtcgacctgcaagcagcttggtgtccacatgacccatgcccgaactcagaag 1326
DB 1251 agaattgcttgctgagcagtagcggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1310
QY 1327 tgaacgcgtagcgccgtagtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1386
DB 1311 tgaacgcgtagcgccgtagtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1370
QY 1387 aggcatacaataaagaaggtcagtcgaaagacttggtgtgtgtgtgtgtgtgtgtgtgt 1446
DB 1371 aggcatacaataaagaaggtcagtcgaaagacttggtgtgtgtgtgtgtgtgtgtgtgt 1430
QY 1447 ttgtcgtgaacgctctcctgtagtagacaatccgcgcggagcgagattgaacgttgcg 1506
DB 1431 ttgtcgtgaacgctctcctgtagtagacaatccgcgcggagcgagattgaacgttgcg 1490
QY 1507 aagcaacgcccggaggtgtgcggtgagcagccgcataaactgtccaggtcacaatt 1566
DB 1491 aagcaacgcccggaggtgtgcggtgagcagccgcataaactgtccaggtcacaatt 1550

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Qy 1567 aagcagaagcgcacccctgacgagatggccttttgcgtttctacaactcttcctgctgc 1626
    |||
Db 1551 aagcagaagcgcacccctgacgagatggccttttgcgtttctacaactcttcctgctgc 1610
Qy 1627 atattcaagaagcgcacccctgacgagatggccttttgcgtttctacaactcttcctgctgc 1686
    |||
Db 1611 atattcaagaagcgcacccctgacgagatggccttttgcgtttctacaactcttcctgctgc 1670
Qy 1687 gcagctat 1694
    |||
Db 1671 gcagctgt 1678

RESULT 12
AAQ83827
ID AAQ83827 standard; DNA: 5110 BP.
XX
AC AAQ83827;
XX
DT 04-OCT-1995 (first entry)
XX
DE Plasmid PCM-T297.
XX
KM Plasmid PCM-T297; bacteriophage T7; RNA polymerase;
XX mutant -11G to T; T7 promoter phi 10; circular; cyclic; ds.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Promoter 198..220
FT /tag= a
FT /note= "Inactive T7 promoter phi 10 mutant (-11G to
    T) prior to a promoterless chloramphenicol
    acetyl transferase gene"
XX
PN US5385834-A.
XX
PD 31-JAN-1995.
XX
PF 13-AUG-1993; 93US-0106433.
XX
PR 13-AUG-1993; 93US-0106433.
XX
PA (GEOR-) GEORGIA TECH RES CORP.
XX
PI Ikeda RA:
XX
DR WPI; 1995-081565/11.
XX
PT New mutant form of T7 RNA polymerase - able to utilize a wide
    range of T7 promoter sequences having mutations that inactivate
    recognition by wild type enzyme
XX
PS Disclosure; Columns 57-62; 79pp; English.
XX
CC AAQ83827 is the plasmid PCM-T297, it was used in the production of
    the bacteriophage T7 RNA polymerase mutant promoter phi 10 -11G
    to T substitution (claimed).
XX
SQ Sequence 5110 BP; 1305 A; 1288 C; 1288 G; 1229 T; 0 other:

Query Match 22.5%; Score 404; DB 16; Length 5110;
Best Local Similarity 96.5%; Pred. No. 4.9e-78;
Matches 413; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 1267 aaggtctgacctgacgagatgcaagcttgggtccacctgaccccatgcccgaactcagaag 1326
    |||
Db 1251 aagaattgcctggcgagcagtagcgcggtgtgtccacctgaccccatgcccgaactcagaag 1310
Qy 1327 tgaacagccgtagcgcgagatgtagtctgggtctcccatgcccgaagtaggggaactgcc 1386
    |||
Db 1311 tgaacagccgtagcgcgagatgtagtctgggtctcccatgcccgaagtaggggaactgcc 1370

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Qy 1387 aggcatacaataaagcgaagctcagtcgaagaagctgggcttctgattatctgtgtc 1446
    |||
Db 1371 aggcatacaataaagcgaagctcagtcgaagaagctgggcttctgattatctgtgtc 1430
Qy 1447 ttgtcggtgacgctctctctgagtaggacaatacgcgcggagagcttgaacgttgcg 1506
    |||
Db 1431 ttgtcggtgacgctctctctgagtaggacaatacgcgcggagagcttgaacgttgcg 1490
Qy 1507 aagcaacgcccggaggtgtgctggcgagagccgcgcacataactcccaagcatcaatt 1566
    |||
Db 1491 aagcaacgcccggaggtgtgctggcgagagccgcgcacataactcccaagcatcaatt 1550
Qy 1567 aagcagaagcgcacccctgacgagatggccttttgcgtttctacaactcttcctgctgc 1626
    |||
Db 1551 aagcagaagcgcacccctgacgagatggccttttgcgtttctacaactcttcctgctgc 1610
Qy 1627 atattcaagaagcgcacccctgacgagatggccttttgcgtttctacaactcttcctgctgc 1686
    |||
Db 1611 atattcaagaagcgcacccctgacgagatggccttttgcgtttctacaactcttcctgctgc 1670
Qy 1687 gcagctat 1694
    |||
Db 1671 gcagctgt 1678

RESULT 13
AAQ83828
ID AAQ83828 standard; DNA: 5110 BP.
XX
AC AAQ83828;
XX
DT 04-OCT-1995 (first entry)
XX
DE Plasmid PCM-P1160.
XX
KM Plasmid PCM-P1160; bacteriophage T7; RNA polymerase;
XX mutant -9C to G; T7 promoter phi 10; circular; cyclic; ds.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Promoter 198..220
FT /tag= a
FT /note= "Inactive T7 promoter phi 10 mutant (-9C to
    G) prior to a promoterless chloramphenicol
    acetyl transferase gene"
XX
PN US5385834-A.
XX
PD 31-JAN-1995.
XX
PF 13-AUG-1993; 93US-0106433.
XX
PR 13-AUG-1993; 93US-0106433.
XX
PA (GEOR-) GEORGIA TECH RES CORP.
XX
PI Ikeda RA:
XX
DR WPI; 1995-081565/11.
XX
PT New mutant form of T7 RNA polymerase - able to utilize a wide
    range of T7 promoter sequences having mutations that inactivate
    recognition by wild type enzyme
XX
PS Disclosure; Columns 63-70; 79pp; English.
XX
CC AAQ83828 is the plasmid PCM-P1160, it was used in the production of
    the bacteriophage T7 RNA polymerase mutant promoter phi 10 -9C
    to G substitution (claimed).
XX
SQ Sequence 5110 BP; 1300 A; 1291 C; 1293 G; 1226 T; 0 other:

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Query Match	22.5%	Score 404	DB 16	Length 5110		
Best Local Similarity	96.5%	Pred. No. 4.9e-78				
Matches 413	Conservative	0	Mismatches 15	Indels 0		
				Gaps 0		
QY 1267	agagtcgacacttcgaagcatcgaagcttggctccacactgaaccatgcccgaatcagaag	1326				
DB 1251	agaatttcctctgcgccgctagcgcggtgtccacactgaccccatgcccgaatcagaag	1310				
QY 1327	tgaaacgcccgtagcgccgatagttagtgggtctcccaatgagagtaggaactgcc	1386				
DB 1311	tgaaacgcccgtagcgccgatagttagtgggtctcccaatgagagtaggaactgcc	1370				
QY 1387	agggcacaataaaacgaaaggctcagtcgaaaggctggcccttcggtttatcgttgt	1446				
DB 1371	agggcacaataaaacgaaaggctcagtcgaaaggctggcccttcggtttatcgttgt	1430				
QY 1447	ttgtcgtgtgaacgctctcctgtagtaggacaatcccgccggagcgagattgaacgttgcg	1506				
DB 1431	ttgtcgtgtgaacgctctcctgtagtaggacaatcccgccggagcgagattgaacgttgcg	1490				
QY 1507	aagcaacggcccgaggggtgtgcgggacgaagcccgccataactgcagcacaataat	1566				
DB 1491	aagcaacggcccgaggggtgtgcgggacgaagcccgccataactgcagcacaataat	1550				
QY 1567	aagcgaagggcatcctctgacgataggccttttgcgtttctcaaaccttctctgcgc	1626				
DB 1551	aagcgaagggcatcctctgacgataggccttttgcgtttctcaaaccttctctgcgc	1610				
QY 1627	atatctacaagccatccccacagatacgcgtaaactagcctcgttttgcatacggaaa	1686				
DB 1611	atatctacaagccatccccacagatacgcgtaaactagcctcgttttgcatacggaaa	1670				
QY 1687	gcagcctat 1694					
DB 1671	gcagcctgt 1678					
RESULT 14						
AA083829						
ID	AA083829 standard; DNA; 5110 BP.					
XX	AA083829;					
AC						
DT	04-OCT-1995 (first entry)					
XX						
DE	Plasmid pCM-T720.					
XX						
KM	Plasmid pCM-T720; bacteriophage T7; RNA polymerase;					
KW	mutant -9C to A; T7 promoter phi 10; circular; cyllic; ds.					
XX						
OS	Synthetic.					
XX						
Key	Location/Qualifiers					
FT	Promoter	198..220				
FT	/*tag= a					
FT	/note= "inactive T7 promoter phi 10 mutant (-9C to					
FT	A) prior to a promoterless chloramphenicol					
FT	acetyl transferase gene"					
XX						
PN	US5385834-A.					
XX						
PD	31-JAN-1995.					
XX						
PF	13-AUG-1993; 93US-0106433.					
XX						
PR	13-AUG-1993; 93US-0106433.					
XX						
PA	(GEOR-) GEORGIA TECH RES CORP.					
XX						
PT	Ikeda RA;					
XX						

DR	WPI: 1995-081565/11.					
XX						
PT	New mutant form of T7 RNA polymerase - able to utilise a wide					
PT	range of T7 promoter sequences having mutations that inactivate					
PT	recognition by wild type enzyme					
XX						
PS	Disclosure: Columns 71-76; 79pp; English.					
XX						
CC	AAO83829 is the plasmid PCM-T270, it was used in the production of					
CC	the bacteriophage T7 RNA polymerase mutant promoter phi 10 -9C					
CC	to A substitution (claimed).					
XX						
SQ	Sequence 5110 BP; 1306 A; 1287 C; 1289 G; 1228 T; 0 other:					
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Query Match	22.5%	Score 404;	DB 16;	Length 5110;		
Best Local Similarity	96.5%;	Pred. No. 4.9e-78;				
Matches 413;	Conservative 0;	Mismatches 15;	Indels 0;	Gaps 0;		
OY	1267	agatgcacgctgcaaggcatgtcaagcttggctccaccctgaccccatacgccaactagaag	1326			
Db	1251	agaatttgtcctggcggaagttagcgcggtgtctccaaacttgacccccatcggaactagaag	1310			
OY	1332	tgaaacgcgcgtatagcgccgatgtttgtgtgggtcttcgccatygagagttaggaactgcc	1386			
Db	1311	tgaaacgcgcgtatagcgccgatgtttgtgtgggtcttcgccatlgagagttaggaactgcc	1370			
OY	1387	aagcgtcaaataaaacggaaggctcagttcgaaaggactggcgcttcgtttactctgtgt	1446			
Db	1371	aggcgtcaaataaaacggaaggctcagttcgaaaggactggcgcttcgtttactctgtgt	1430			
OY	1447	tgtctgtgtgaagcgcctctccgtagttagacaataccgcgcggagcgagattgaacgttcg	1506			
Db	1431	tgtctgtgtgaagcgcctctccgtagttagacaataccgcgcggagcgagattgaacgttcg	1490			
OY	1507	aagcacggtcccgsgaggtgtgcggcgaggaogccgcgaataaactgcagagcataaatt	1566			
Db	1491	aagcacggtcccgsgaggtgtgcggcgaggaogccgcgaataaactgcagagcataaatt	1550			
OY	1567	aagcgaaagccatctctgacggatggccttttgcgtttctatacaacttctctgtgtc	1626			
Db	1551	aagcgaaagccatctctgacggatggccttttgcgtttctatacaacttctctgtgtc	1610			
OY	1627	atatctacaagcattccccccacagatacgtgtaacctagcctgttttgcatacggaaa	1686			
Db	1611	atatctacaagcattccccccacagatacgtgtaacctagcctgttttgcatacggaaa	1670			
OY	1687	gcagcctat 1694 				
Db	1671	gcagcctgt 1678				
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RESULT 15						
ID	AAO83830 standard; DNA; 5110 BP.					
XX						
AC	AAO83830;					
XX						
DT	05-OCT-1995 (first entry)					
XX						
DE	Plasmid pcm-p1087.					
XX						
KM	Plasmid pcm-p1087; bacteriophage T7; RNA polymerase;					
XX	mutant -9C to T; T7 promoter phi 10; circular; cyclic; ds.					
OS	Synthetic.					
XX						
FH	Key Location/Qualifiers					
FT	Promoter 198..220					
FT	/tag= "a					
FT	/note= "Inactive T7 promoter phi 10 mutant (-9C to					
FT	T) prior to a promoterless chloramphenicol					
FT	acetyl transferase gene"					

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XX US5385834-A.
PN
XX
XX 31-JAN-1995.
PD
XX
XX 13-AUG-1993; 93US-0106433.
PE
XX
XX 13-AUG-1993; 93US-0106433.
PR
XX
XX 13-AUG-1993; 93US-0106433.
PA
XX (GEOR-) GEORGIA TECH RES CORP.
PI Ikeda RA;
XX
XX WPI; 1995-081565/11.
DR
XX
XX New mutant form of T7 RNA polymerase - able to utilise a wide
PT range of T7 promoter sequences having mutations that inactivate
PT recognition by wild type enzyme
XX
XX Disclosure: Columns 77-83; 79pp; English.
PS
XX
XX AA083830 is the plasmid PCM-P1087, it was used in the production of
CC the bacteriophage T7 RNA polymerase mutant promoter phi 10 -9C
CC to T substitution (claimed).
XX
XX Sequence 5110 BP; 1305 A; 1287 C; 1289 G; 1229 T; 0 other;
SQ

Query Match 22.5%; Score 404; DB 16; Length 5110;
Best Local Similarity 96.5%; Pred. No. 4.9e-78;
Matches 413; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1267 agagtcgacctgcaaggcatgcaagcttgggtccacctgaccccatgccaactcagaag 1326
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Db 1251 agaatttcgctgcgcgtagcgcgctgctgcgcacccatgccaactcagaag 1310

QY 1327 tgaacgcgcgtatagccgcatgtatgtgtggtctcccatgagtaggaactgcc 1386
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1311 tgaacgcgcgtatagccgcatgtatgtgtggtctcccatgagtaggaactgcc 1370

QY 1387 aggcataataaagcaagagctcagtcgaaagactggccttcgttttactctgt 1446
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1371 aggcataataaagcaagagctcagtcgaaagactggccttcgttttactctgt 1430

QY 1447 ttgtcgtgtaacgctctcctcgtatggaacaaatccgcggaagcgatltgaaagtlgcg 1506
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1431 ttgtcgtgtaacgctctcctcgtatggaacaaatccgcggaagcgatltgaaagtlgcg 1490

QY 1507 aagcaacgccccgaggggtgtggtggcgaagacccgcataactgcagcatcaatt 1566
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1491 aagcaacgccccgaggggtgtggtggcgaagacccgcataactgcagcatcaatt 1550

QY 1567 aagcagaagccatcctgaagatgaccttttgcgtttctacaactcttcctgtc 1626
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1551 aagcagaagccatcctgaagatgaccttttgcgtttctacaactcttcctgtc 1610

QY 1627 atatctacaagccatccccccacagatacgtlaaactagcctcgttttgcacacagaaa 1686
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1611 atatctacaagccatccccccacagatacgtlaaactagcctcgttttgcacacagaaa 1670

QY 1687 gcaagctat 1694
   ||||| |||
Db 1671 gcaagctgt 1678
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Job time: 7667 sec